

#10

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SEQUENCE LISTING

<110> Fouser, Lynette
Liu, Wei
Deng, Bija

<120> TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING
SAME

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<141> 2002-01-14

<150> 60/261442
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<150> 60/267021
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25

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Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
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Glu Arg Cys Val Glu Ile Pro
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ctactatacc gagttttat aattaacaat tcactagaaa aggagcaaaa gtttatgaa 660
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Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Met Phe Ser Cys Ser Met Lys Ser Ser His Gln Lys Pro Ser
65 70 75 80

Gly Cys Trp Gln His Ile Ser Cys Asn Phe Pro Gly Cys Arg Thr Leu
85 90 95

Ala Lys Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
100 105 110

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
115 120 125

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
130 135 140

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
145 150 155 160

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
165 170 175

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
180 185 190

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
195 200 205

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
210 215 220

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
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Glu Arg Cys Val Glu Ile Pro
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actcaagaac tctcttgcata ccttaccagt gaaacctcag acatacagga accttattac 300
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Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Arg Ala Lys
115 120 125

Gly Leu
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 <213> Artificial Sequence

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 Asn Phe Arg Ser Val Leu Leu Trp Asp Pro Pro Gly Val Arg Lys Gly
 35 40 45

 Asn Leu Ser Tyr Thr Val Gln Ala Lys Ser Ile Phe Pro Lys Gln Asn
 50 55 60

 Phe Asn Asn Val Thr Thr Asn Leu Asn Val Thr Glu Cys Asp Val Ser
 65 70 75 80

 Ser Leu Ser Val Tyr Gly Ala Tyr Val Leu Arg Val Arg Thr Glu Trp
 85 90 95

 Glu Asp Glu His Ser Asp Trp Ala Val Val Arg Phe Lys Pro Met Ala
 100 105 110

 Asp Thr Val Ile Gly Pro Pro Ser Val Asn Val Lys Ser Glu Ser Gly
 115 120 125

 Thr Leu His Val Asp Phe Thr Gly Pro Ala Ala Asp Arg Glu His Asp
 130 135 140

 Lys Trp Ser Leu Lys Gln Tyr Tyr Gly Ser Trp Ile Tyr Arg Ile Leu
 145 150 155 160

 Tyr Trp Lys Lys Gly Ser Asn Lys Lys Val Ile His Ile Asp Thr Lys
 165 170 175

 His Asn Ser Glu Ile Leu Ser Gln Leu Glu Pro Trp Thr Ile Tyr Cys
 180 185 190

 Ile Gln Val Gln Gly Val Ile Pro Glu Trp Asn Lys Thr Gly Glu Arg
 195 200 205

Ser Gln Glu Leu Cys Glu Gln Thr Thr His Asn Gly Val Thr Pro Val
210 215 220

Trp Ile Val Val Thr Val Leu Leu Gly Ser Met Leu Ala Val Ile Ile
225 230 235 240

Ser Val Pro Val Cys Phe Phe Ala Phe Trp Tyr Leu Tyr Arg Phe Thr
245 250 255

Lys His Val Phe Phe Pro Ser Tyr Ile Phe Pro Gln His Leu Lys Glu
260 265 270

Phe Phe Ser Pro Val Pro Gln Glu Glu His His Phe His Asp Trp Leu
275 280 285

Thr Val Ile Ser Glu Glu Pro Lys Ser Gln Arg Asp Glu Thr Val Glu
290 295 300

Glu Ala Ser Arg Thr Ala Glu His His Gln Asp Ser Lys Gln Glu Ile
305 310 315 320

Ser Asp Ser Glu Ile Leu Pro Pro Leu Glu Arg Asp Gln Thr Leu Leu
325 330 335

Thr Leu Gln Ser Gly
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<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 9
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cgccccagaa ggtccgattt cagttccagaa attttcacaa tattttgcac tggcaagcag 180
ggagctctt ccccaagcaac aacagcatct actttgtgcac gtacaagatg tatggacaga 240
gccaatggga agataaaagtt gactgctggg ggaccacggc gctcttctgt gacctgacca 300
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gccactctgc ctggaccagg acaccccgct tcactccatg gtggaaaca aaactagatc 420
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ctcagagagc tggtaaattt gaaggtctga tacctcattc cagctactgc gtatgtggctg 660
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Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln Ala
35 40 45

Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr Lys
50 55 60

Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly Thr
65 70 75 80

Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr Glu
85 90 95

Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser Ala
100 105 110

Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu Asp
115 120 125

Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val Leu
130 135 140

Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn Ala
145 150 155 160

Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile Asn
165 170 175

Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg Ala
180 185 190

Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val Ala
195 200 205

Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys Glu
210 215 220

Arg Cys Val Gln Ile Pro
225 230

<210> 13

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<222> (7)

<223> Wherein X is the amino acid L or F

<220>

<221> VARIANT

<222> (10)

<223> Wherein X is the amino acid L or F

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<210> 14

<211> 15

<212> PRT

<213> human

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<221> VARIANT

<222> (11)

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<220>

<221> VARIANT

<222> (14)

<223> Wherein X is the amino acid A or P

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<210> 15

<211> 15

<212> PRT

<213> human

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<220>
<221> VARIANT
<222> (9)
<223> Wherein X is the amino acid M or I

<220>
<221> VARIANT
<222> (13)
<223> Wherein X is the amino acid S or R

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<210> 16
<211> 16
<212> PRT
<213> human

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<210> 17
<211> 21
<212> PRT
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<220>
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<220>
<221> VARIANT
<222> (18)
<223> Wherein X is the amino acid A or V

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Lys Xaa Tyr Glu Gly
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<213> human

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<220>
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<220>
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<223> Wherein X is the amino acid M or I

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<210> 19
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<213> human

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<220>
<221> VARIANT
<222> (13)
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<210> 20
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<212> PRT
<213> human

<400> 20

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
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Thr Gly Val Ala Gly Thr Asn Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

<210> 21
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<213> human

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20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

<210> 22

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<213> human

<400> 22

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 20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

Glu Arg Cys Val Glu Ile Pro
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 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
 65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
 85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
 100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
 115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
 130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
 145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
 165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
 180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
 195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
 210 215 220

Glu Arg Cys Val Glu Ile Pro
 225 230

<210> 24
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 <213> human

<400> 24
 Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
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Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu His Pro Gln
 20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
 35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
 50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly

65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

<210> 25
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<213> human

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Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
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Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

Lys Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
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Glu Arg Cys Val Glu Ile Pro
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<210> 26

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<400> 26

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
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Arg Val Gln Phe Gln Ser Arg Gln Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

<210> 27

<211> 231

<212> PRT

<213> human

<400> 27

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Val Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn

145	150	155	160
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile			
165	170	175	
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg			
180	185	190	
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val			
195	200	205	
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu			
210	215	220	
Glu Arg Cys Val Glu Ile Pro			
225	230		
<210> 28			
<211> 231			
<212> PRT			
<213> human			
<400> 28			
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu			
1	5	10	15
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln			
20	25	30	
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln			
35	40	45	
Pro Gly Arg Leu Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr			
50	55	60	
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly			
65	70	75	80
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln			
85	90	95	
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser			
100	105	110	
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile			
115	120	125	
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val			
130	135	140	
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn			
145	150	155	160
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile			
165	170	175	

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

<210> 29
<211> 231
<212> PRT
<213> human

<400> 29
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Ala Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

<210> 30
<211> 231
<212> PRT
<213> human

<400> 30
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Ile Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro

225

230

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 31
gaattcgtcg acccaccatg cctaaggcatt gccttc

36

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 32
tggaatctgc acacatctct cc

22

<210> 33
<211> 199
<212> PRT
<213> human

<220>
<221> VARIANT
<222> (139)
<223> Wherein "X" is a space inserted in the Blast alignment analysis.

<400> 33
Lys Pro Gln Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu
1 5 10 15

Gln Trp Gln Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe
20 25 30

Val Gln Tyr Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp
35 40 45

Cys Trp Gly Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser
50 55 60

Asp Ile Gln Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly
65 70 75 80

Ser Tyr Ser Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu
85 90 95

Thr Lys Ile Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser
 100 105 110
 Leu Leu Val Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys
 115 120 125
 Glu Lys Asn Val Ser Ile Glu Asp Tyr Tyr Xaa Glu Leu Leu Tyr Arg
 130 135 140
 Val Phe Ile Ile Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu
 145 150 155 160
 Gly Ala His Arg Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser
 165 170 175
 Tyr Cys Val Val Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser
 180 185 190
 Gln Arg Ser Glu Glu Arg Cys
 195

<210> 34
 <211> 231
 <212> PRT
 <213> human

<400> 34
 Ser Met Met Pro Lys His Cys Leu Leu Gly Leu Leu Ile Ile Leu Leu
 1 5 10 15
 Ser Ser Ala Thr Glu Ile Gln Pro Ala Arg Val Ser Leu Thr Pro Gln
 20 25 30
 Lys Val Arg Phe Gln Ser Arg Asn Phe His Asn Ile Leu His Trp Gln
 35 40 45
 Ala Gly Ser Ser Leu Pro Ser Asn Asn Ser Ile Tyr Phe Val Gln Tyr
 50 55 60
 Lys Met Tyr Gly Gln Ser Gln Trp Glu Asp Lys Val Asp Cys Trp Gly
 65 70 75 80
 Thr Thr Ala Leu Phe Cys Asp Leu Thr Asn Glu Thr Leu Asp Pro Tyr
 85 90 95
 Glu Leu Tyr Tyr Gly Arg Val Met Thr Ala Cys Ala Gly Arg His Ser
 100 105 110
 Ala Trp Thr Arg Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Leu
 115 120 125
 Asp Pro Pro Val Val Thr Ile Thr Arg Val Asn Ala Ser Leu Arg Val
 130 135 140
 Leu Leu Arg Pro Pro Glu Leu Pro Asn Arg Asn Gln Ser Gly Lys Asn
 145 150 155 160

Ala Ser Met Glu Thr Tyr Tyr Gly Leu Val Tyr Arg Val Phe Thr Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Ala Tyr Glu Gly Thr Gln Arg
180 185 190

Ala Val Glu Ile Glu Gly Leu Ile Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Met Tyr Gln Pro Met Phe Asp Arg Arg Ser Pro Arg Ser Lys
210 215 220

Glu Arg Cys Val Gln Ile Pro
225 230

<210> 35

<211> 231

<212> PRT

<213> human

<400> 35

Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15

Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg

180

185

190

Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
210 215 220

Glu Arg Cys Val Glu Ile Pro
225 230

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 36
cttgcaacca ttaggcctaa acattgc

27

<210> 37
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 37
atgatgccta aacattgctt tctagg

26

<210> 38
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 38
ggaactctgg ttgccagaca agcacac

27

<210> 39
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR Primer

<400> 39

caaggagaga tgtgtgcaga ttccatga

28